

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09328574

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5\* amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ✓ Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,574

DATE: 09/07/2001

TIME: 16:45:43

Input Set : A:\UCSD1310-1.ST25.txt

Output Set: N:\CRF3\09072001\I828574.raw

See page 4 of 7

2 <110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
 3 ALBANI, Salvatore  
 4 PRAKKEN, Berent  
 6 <120> TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF  
 8 <130> FILE REFERENCE: UCSD1310-1  
 10 <140> CURRENT APPLICATION NUMBER: US 09/828,574  
 11 <141> CURRENT FILING DATE: 2001-04-06  
 13 <150> PRIOR APPLICATION NUMBER: US 60/224,104  
 14 <151> PRIOR FILING DATE: 2000-08-09  
 16 <160> NUMBER OF SEQ ID NOS: 13  
 18 <170> SOFTWARE: PatentIn version 3.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 573  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Homo sapiens  
 25 <400> SEQUENCE: 1  
 27 Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg  
 28 1 5 10 15  
 30 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe  
 31 20 25 30  
 33 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
 34 35 40 45  
 36 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile  
 37 50 55 60  
 39 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val  
 40 65 70 75 80  
 42 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys  
 43 85 90 95  
 45 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly  
 46 100 105 110  
 48 Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe  
 49 115 120 125  
 51 Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val  
 52 130 135 140  
 54 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys  
 55 145 150 155 160  
 57 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala  
 58 165 170 175  
 60 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys  
 61 180 185 190  
 63 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn  
 64 195 200 205  
 66 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile  
 67 210 215 220  
 69 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln  
 70 225 230 235 240  
 72 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

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Input Set : A:\UCSD1310-1.ST25.txt

Output Set: N:\CRF3\09072001\I828574.raw

```

73           245           250           255
75 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
76           260           265           270
78 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
79           275           280           285
81 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
82           290           295           300
84 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
85 305           310           315           320
87 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
88           325           330           335
90 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
91           340           345           350
93 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
94           355           360           365
96 Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
97           370           375           380
99 Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
100 385           390           395           400
102 Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
103           405           410           415
105 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
106           420           425           430
108 Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
109           435           440           445
111 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
112           450           455           460
114 Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
115 465           470           475           480
117 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
118           485           490           495
120 Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
121           500           505           510
123 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
124           515           520           525
126 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
127           530           535           540
129 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
130 545           550           555           560
132 Met Gly Gly Met Gly Gly Gly Met Gly Gly Met Phe
133           565           570
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 15
137 <212> TYPE: PRT
138 <213> ORGANISM: Mycobacterium
140 <400> SEQUENCE: 2
142 Gly Glu Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr
143 1           5           10           15
145 <210> SEQ ID NO: 3

```

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```

146 <211> LENGTH: 15
147 <212> TYPE: PRT
148 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 3
152 Gly Glu Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly
153 1 5 10 15
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 15
157 <212> TYPE: PRT
158 <213> ORGANISM: Mycobacterium
160 <400> SEQUENCE: 4
162 Pro Tyr Ile Leu Leu Val Ser Ser Lys Val Ser Thr Val Lys Asp
163 1 5 10 15
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 15
167 <212> TYPE: PRT
168 <213> ORGANISM: Homo sapiens
170 <400> SEQUENCE: 5
172 Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
173 1 5 10 15
175 <210> SEQ ID NO: 6
176 <211> LENGTH: 15
177 <212> TYPE: PRT
178 <213> ORGANISM: Mycobacterium
180 <400> SEQUENCE: 6
182 Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys
183 1 5 10 15
185 <210> SEQ ID NO: 7
186 <211> LENGTH: 15
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 7
192 Lys Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys
193 1 5 10 15
195 <210> SEQ ID NO: 8
196 <211> LENGTH: 15
197 <212> TYPE: PRT
198 <213> ORGANISM: Mycobacterium
200 <400> SEQUENCE: 8
202 Ile Ala Gly Leu Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys
203 1 5 10 15
205 <210> SEQ ID NO: 9
206 <211> LENGTH: 15
207 <212> TYPE: PRT
208 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 9
212 Val Ala Ser Leu Leu Thr Thr Ala Glu Val Val Val Thr Glu Ile
213 1 5 10 15
215 <210> SEQ ID NO: 10

```

## RAW SEQUENCE LISTING

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Input Set : A:\UCSD1310-1.ST25.txt

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216 <211> LENGTH: 15  
 217 <212> TYPE: PRT  
 218 <213> ORGANISM: synthetic construct *Entered*  
 220 <400> SEQUENCE: 10  
 222 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu *Valid 213 responses are only "Artificial Sequence", "Unknown" or the name of some specific species*  
 223 1 5 10 15  
 225 <210> SEQ ID NO: 11  
 226 <211> LENGTH: 15  
 227 <212> TYPE: PRT  
 228 <213> ORGANISM: synthetic construct  
 230 <400> SEQUENCE: 11  
 232 Asp Glu Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu  
 233 1 5 10 15  
 235 <210> SEQ ID NO: 12  
 236 <211> LENGTH: 11  
 237 <212> TYPE: PRT *Entered*  
 238 <213> ORGANISM: synthetic construct  
 240 <220> FEATURE:  
 241 <221> NAME/KEY: VARIANT  
 242 <222> LOCATION: (2)..(2)  
 243 <223> OTHER INFORMATION: Xaa is any amino acid  
 246 <400> SEQUENCE: 12  
 W--> 248 Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala  
 249 1 5 10  
 251 <210> SEQ ID NO: 13  
 252 <211> LENGTH: 573  
 253 <212> TYPE: PRT  
 254 <213> ORGANISM: Homo sapiens  
 256 <400> SEQUENCE: 13  
 258 Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg  
 259 1 5 10 15  
 261 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe  
 262 20 25 30  
 264 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
 265 35 40 45  
 267 Asp Ala Val Ala Val Thr Met Glu Pro Lys Gly Arg Thr Val Ile Ile  
 268 50 55 60  
 270 Glu Gln Ser Trp Gly Ser Pro Asn Val Thr Lys Asp Gly Val Thr Val  
 271 65 70 75 80  
 273 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys  
 274 85 90 95  
 276 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ser Gly Asp Gly  
 277 100 105 110  
 279 Thr Thr Thr Ala Thr Val Leu Ala Gly Ser Ile Ala Lys Glu Gly Phe  
 280 115 120 125  
 282 Gln Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val  
 283 130 135 140  
 285 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys  
 286 145 150 155 160

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 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

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```

288 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Met Ile Ser Ala
289           165           170           175
291 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
292           180           185           190
294 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
295           195           200           205
297 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
298           210           215           220
300 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
301 225           230           235           240
303 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Val Gln Ser
304           245           250           255
306 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His His Lys Pro Leu Val
307           260           265           270
309 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Ile Leu
310           275           280           285
312 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
313           290           295           300
315 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
316 305           310           315           320
318 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
319           325           330           335
321 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
322           340           345           350
324 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Leu Glu
325           355           360           365
327 Lys Arg Ile Gln Glu Ile Ile Gly Gln Leu Asp Val Thr Thr Ser Glu
328           370           375           380
330 Tyr Glu Lys Glu Lys Leu Asn Glu Trp Leu Ala Lys Leu Ser Asp Gly
331 385           390           395           400
333 Val Val Val Leu Lys Phe Gly Gly Thr Ser Asp Val Glu Val Asn Glu
334           405           410           415
336 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
337           420           425           430
339 Glu Gly Gly Ile Val Leu Gly Gly Gly Phe Ala Leu Leu Arg Cys Ile
340           435           440           445
342 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
343           450           455           460
345 Met Glu Ile Val Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Thr Ala
346 465           470           475           480
348 Thr Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
349           485           490           495
351 Asn Ser Ser Glu Val Gly Tyr Asp Ala Met Val Gly Asp Phe Met Asn
352           500           505           510
354 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Leu Val Arg Thr Ala
355           515           520           525
357 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
358           530           535           540
360 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala

```

VERIFICATION SUMMARY

PATIENT APPLICATION: US/09/828,574

DATE: 09/07/2001

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Input Set : A:\UCSD1310-1.ST25.txt

Output Set: N:\CRF3\09072001\I828574.raw

L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12